

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 17, 2003, 16:37:52 ; Search time 32 Seconds
(without alignments)
1674.133 Million cell updates/sec

Title: US-09-840-243B-11

Perfect score: 1341
Sequence: 1 MELTPAEDLIQTQTPASE.....VIENHLKLFQSNVPADE 260

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL 21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriophage: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	621.5	46.3	313	4 Q9H9E1	Q9H9E1 homo sapien
2	612.5	45.7	312	11 Q99PE2	Q99PE2 mus musculu
3	439	32.7	154	11 Q9D1J8	Q9D1J8 mus musculu
4	274	20.4	234	5 Q9VLS8	Q9VLS8 drosophila
5	219.5	16.4	426	16 Q8YTG9	Q8YTG9 arabidosa sp
6	214	16.0	1786	5 Q17344	Q17344 caenorhabdi
7	214	16.0	1809	5 Q17487	Q17487 caenorhabdi
8	214	16.0	1815	5 Q17488	Q17488 caenorhabdi
9	214	16.0	1867	5 Q17489	Q17489 caenorhabdi
10	214	16.0	2039	5 Q17489	Q17489 caenorhabdi
11	214	16.0	6994	5 Q17343	Q17343 caenorhabdi
12	212	15.8	1762	11 Q9E0G6	Q9E0G6 rattus norv
13	212	15.8	1777	4 Q9UJH0	Q9UJH0 homo sapien
14	210.5	15.7	1159	5 Q9NCP8	Q9NCP8 drosophila
15	210.5	15.7	1599	11 Q99NH0	Q99NH0 mus musculu
16	210.5	15.7	2443	5 Q9VSA2	Q9VSA2 drosophila

17	207.5	15.5	1031	4 Q9UF42	Q9UF42 homo sapien
18	207.5	15.5	1715	11 Q9ERD4	Q9ERD4 rattus norv
19	207.5	15.4	598	11 Q9CUB2	Q9CUB2 mus musculu
20	206.5	15.4	552	4 Q9CUF1	Q9CUF1 homo sapien
21	206.5	15.4	719	4 Q9EF53	Q9EF53 homo sapien
22	206.5	15.4	917	4 Q9EKH4	Q9EKH4 homo sapien
23	205.5	15.3	342	5 Q9V0I1	Q9V0I1 drosophila
24	205.5	15.3	655	11 Q9CZK6	Q9CZK6 mus musculu
25	201	15.0	616	4 Q96GK0	Q96GK0 homo sapien
26	199	14.8	1498	5 Q9W2I1	Q9W2I1 drosophila
27	198	14.8	627	4 Q8WY90	Q8WY90 homo sapien
28	198	14.8	627	4 Q8WY90	Q8WY90 homo sapien
29	198	14.8	4001	5 Q8WY90	Q8WY90 homo sapien
30	197	14.7	686	4 Q8WY90	Q8WY90 homo sapien
31	197	14.7	843	11 P97582	P97582 rattus norv
32	195.5	14.6	456	10 Q9SR03	Q9SR03 arbidopsis
33	195.5	14.5	435	4 Q9HA95	Q9HA95 homo sapien
34	193	14.4	435	4 Q9HA95	Q9HA95 mus musculu
35	193	14.4	2622	11 Q70511	Q70511 rattus norv
36	192	14.4	4377	4 Q12955	Q12955 homo sapien
37	192	14.3	532	4 Q8VHF9	Q8VHF9 rattus norv
38	192	14.3	532	4 Q8VHF9	Q8VHF9 rattus norv
39	191	14.2	1856	4 Q9GM49	Q9GM49 macaca fasc
40	191	14.2	1856	4 Q9GM49	Q9GM49 macaca fasc
41	190	14.2	460	4 Q9H6J9	Q9H6J9 homo sapien
42	189	14.2	784	5 Q9VCA7	Q9VCA7 drosophila
43	189	14.1	627	4 Q96G77	Q96G77 homo sapien
44	189	14.1	1001	4 Q14349	Q14349 homo sapien
45	189	14.1	1001	4 Q9U0L8	Q9U0L8 homo sapien

ALIGNMENTS

RESULT 1	Q9H9E1	PRELIMINARY;	PRT;	313 AA.
AC	Q9H9E1			
DT	01-MAR-2001 (TREMBL)	16, Created		
DT	01-MAR-2001 (TREMBL)	16, Last sequence update		
DT	01-JUN-2002 (TREMBL)	21, Last annotation update		
DE	CDNA FLJ12814 fis, clone NT2R2002520, weakly similar to Homo sapiens			
DE	transcription factor RFX-B (RFXB) mRNA (Ankyrin) (Ankyrin-repeat			
DE	family A protein 2) (Hypothetical 34.3 kDa protein).			
GN	ANKRA2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Isoqal T., Oca T., Hayaishi K., Sugiyama T., Otsuki T., Suzuki Y.,			
RA	Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,			
RA	Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,			
RA	Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto U.,			
RA	Wakematsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.,			
RT	"NEO human cDNA sequencing project";			
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RA	Mao Y., Xie Y., Zhou Z., Zhao W., Zhao S., Wang W., Huang Y., Wang S.,			
RA	Tang R., Chen X., Wu C.,			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=20422473; PubMed=10965114;			
RA	Radner K., Boyer A.D., Fargnhar M.G., Arden K.C.,			
RT	"Assignment of ankyrin repeat, family A (RFXANK-like) 2 (ANKRA2) to			
RT	human chromosome 5q12--q13 by radiation hybrid mapping and somatic			
RT	cell hybrid PCR."			
RL	Cytogenet. Cell Genet. 89:164-165(2000).			
RL	[4]			
RP	SEQUENCE FROM N.A.			

RA Rader K.A., Orlando R.A., Lou X., Farquhar M.G.;
 RT "Characterization of ANKRA, a novel ankyrin repeat protein that
 interacts with the cytoplasmic domain of megalin.";
 RL J. Am. Soc. Nephrol. 11:0-0(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Strausberg R.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK022876; BAB14288.1; -
 DR EMBL; AF251051; AKK34841.1; -
 DR EMBL; AF314032; AKK01621.1; -
 DR EMBL; BC012917; AAH12917.1; -
 DR HSSP; P80144; 2MYO.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 3.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 3.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR ANK repeat; Hypothetical protein; Repeat.
 KW ANK repeat; Repeat.
 SQ SEQUENCE 313 AA; 34272 MW; 31653B10B4DE61 CRC64;

Query Match 46.3%; Score 621.5; DB 4; Length 313;
 Best Local Similarity 60.6%; Pred. No. 2.9e-44;
 Matches 126; Conservative 26; Mismatches 49; Indels 7; Gaps 2;

QY 51 NEPDASV-----SSPDAGSLKSTLTITNQRGNVSALPATLDSLSHOLAAGELD 104
 Db 104 SPSFGIOVRHYVTPSTTKHSPKOSTTITNKRGNVSTTPLLANSLSAHOLAAGEL 163
 QY 105 QKEHLRKGDNLVKNPDERGFTPLIWASAFGEIETVRFLLEWGADPHILAKERESALSLA 164
 Db 164 YLATRIEQ-ENVINHTDEGFTPLMMAAHGQIAVVEFLQNGADPQLGKGRESALSLA 222
 QY 165 STGYTDIVGLLEKRDVINTIDMNGGTPLLVAVRGNHVKCVALLARGADLTTEADSGY 224
 Db 223 CSKGYTDIVKMLDGCVDVNEIDMNGGTPLLVAVRGNHVKCVALLARGADLTTEADSGY 282
 QY 225 TPMDLAVALGVRKVOQVNIENHILKLFQS 252
 Db 283 NSMDLAVALGYRVOQVNIENHILKLFQS 310

RESULT 2

Q99PE2 PRELIMINARY; PRT; 312 AA.

AC Q99PE2
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Ankyrin-repeat family A protein.
 GN ANKRA2 OR 1110004M18RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20422473; Pubmed=10965114;
 RA Rader K., Boyer A.D., Farquhar M.G., Arden K.C.;
 RT "Assignment of ankyrin repeat, family A (ANKRA-1like) 2 (ANKRA2) to
 human chromosome 5q12-->q13 by radiation hybrid mapping and somatic
 cell hybrid PCR.";
 RL Cytogenet. Cell Genet. 89:164-165(2000).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20547411; Pubmed=11095640;
 RA Rader K., Orlando R.A., Lou X., Farquhar M.G.;
 RT "Characterization of ANKRA, a novel ankyrin repeat protein that
 interacts with the cytoplasmic domain of megalin.";
 RL J. Am. Soc. Nephrol. 11:2167-2178(2000).
 DR EMBL; AF314031; AKK01620.1; -

DR HSSP; P80144; 2MYO.
 DR MGD; MGI:1915808; Ankra2.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 3.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 3.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR ANK repeat; Repeat.
 KW ANK repeat; Repeat.
 SQ SEQUENCE 312 AA; 34062 MW; 3B52B1415B7A5AFA CRC64;

Query Match 45.7%; Score 612.5; DB 11; Length 312;
 Best Local Similarity 60.1%; Pred. No. 1.7e-43;
 Matches 125; Conservative 25; Mismatches 51; Indels 7; Gaps 2;

QY 51 NEPDASV-----SSPDAGSLKSTLTITNQRGNVSALPATLDSLSHOLAAGELD 104
 Db 103 SPSFGIOVRHYVTPSTTKHSPKOSTTITNKRGNVSTTPLLANSLSAHOLAAGEL 162
 QY 105 QKEHLRKGDNLVKNPDERGFTPLIWASAFGEIETVRFLLEWGADPHILAKERESALSLA 164
 Db 163 YLATRIEQ-ENVINHTDEGFTPLMMAAHGQIAVVEFLQNGADPQLGKGRESALSLA 221
 QY 165 STGYTDIVGLLEKRDVINTIDMNGGTPLLVAVRGNHVKCVALLARGADLTTEADSGY 224
 Db 222 CSKGYTDIVKMLDGCVDVNEIDMNGGTPLLVAVRGNHVKCVALLARGADLTTEADSGY 281
 QY 225 TPMDLAVALGVRKVOQVNIENHILKLFQS 252
 Db 282 NSMDLAVALGYRVOQVNIENHILKLFQS 309

RESULT 3

Q9D1J8 PRELIMINARY; PRT; 154 AA.

AC Q9D1J8
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 1110004M18RIK protein.
 GN ANKRA2 OR 1110004M18RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; Pubmed=11217851;
 RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
 RA Brownstein M.O., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK003438; BAB22790.1; -
 DR HSSP; P80144; 2MYO.
 DR MGD; MGI:1915808; Ankra2.
 DR InterPro; IPR002110; ANK.

DR Pfam: PF00023; ank: 3.
 DR PRINTS: PR01415; ANKYRIN.
 DR SMART: SM00248; ANK: 3.
 DR PROSITE: PS50088; ANK_REPEAT: 3.
 DR PROSITE: PS50297; ANK_REGION: 1.
 DR ANK repeat: Repeat.
 SQ SEQUENCE 154 AA; 16701 MW; 95E966FP4CF0B69A CRC64;
 Query Match 32.7%; Score 439; DB 11; Length 154;
 Best Local Similarity 68.3%; Pred. No. 2, 4e-29;
 Matches 84; Conservative 13; Mismatches 26; Indels 0; Gaps 0;
 QY 114 DNIWPKDERGFTPLIWASAFGEIETVRFLBEGADPHILAKERESALSLASTGCTYDIV 173
 DB 11 ENVIHTDEGFTPLWMAAHGQIAVVEFLQNGADPOLLGKRESALSLASTGCTYDIV 70
 QY 174 GLLLEDDVDINIDMNGCTFLLYAVRGNHYKCVALLARGLDITTEADSGYTPMDLAVAL 233
 DB 71 KMLDGVGVNEYDMNGTFLLYAVHGNHYKCVKMLLENGADFTITETDSGYNSMDLAVAL 130
 QY 234 GYR 236
 DB 131 GYR 133
 RESULT 4
 QYVL58 PRELIMINARY; PRT: 234 AA.
 AC 09VL58; (TREMBlrel. 13, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE CGS846 protein (LP07441p).
 GN CGS846
 OS Drosophila melanogaster (Fruit fly)
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_Taxid=7227;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=BERKELEY;
 RX MEDLINE=20196006; Pubmed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.C., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Ballw R.M., Baatu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Durbin K., Doup L.E., Dowes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferrar C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Giodes A., Gong F., Gottrell J.H., Gu Z., Guan F., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 RA Jalali M., Kalush F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Klup D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mantei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mervulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson S.R., Nelson K.A., Nixon K., Nuskern D.R., Paclab J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton W., Strong R., Sun E.,

RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guatini H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Paclab J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF003626; AAF52838.2;
 DR EMBL: AY061547; AAL29095.1;
 DR HSSP: P80144; 2MYO.
 DR FlyBase: FBgn0032171; CGS846.
 DR InterPro: IPR002110; ANK.
 DR Pfam: PF00023; ank: 4.
 DR PRINTS: PR01415; ANKYRIN.
 DR SMART: SM00248; ANK: 3.
 DR PROSITE: PS50088; ANK_REPEAT: 2.
 DR PROSITE: PS50297; ANK_REGION: 1.
 DR ANK repeat: Repeat.
 SQ SEQUENCE 234 AA; 24838 MW; A4E8DFB79BF0514 CRC64;
 Query Match 20.4%; Score 274; DB 5; Length 234;
 Best Local Similarity 33.8%; Pred. No. 3, 6e-15;
 Matches 80; Conservative 37; Mismatches 96; Indels 24; Gaps 6;
 QY 13 TQTPASELGDPDPGEAAGSDTAVLSLFPCTPPVNPBPASVSSPOAGSLKSTT 72
 DB 7 TQTPAN---SDDEGVRAPTSMVLVDKRAFLPYRQ-----STV 47
 QY 73 LTRNRGN-EVSAIPATLDSLTHQAQGL--DQKEHLRGDNIWPKDERGFTPLI 129
 DB 48 LTNLRGNTEATFCPEV-SLSPHERAGGEITEGVAAERAAQONIDYK-DAHGFALH 105
 QY 130 WASAFGEIETVRFLBEGADPHILAKERESALSLASTGCTYDIVGLLLEDDVDINIDM 189
 DB 106 WASVQQLVSVQLVAAGANVNTMAEDLISPLLAAGGHNELVFLBEGADSGHMDIV 165
 QY 190 GGPFLYAVRGNHYKCVALLARGLDITTEADSGYTPMDLAVALGYRKYQVNIENHI 246
 DB 166 GNTALWYMAAHGQIAVVEFLQNGADPOLLGKRESALSLASTGCTYDIV 222
 RESULT 5
 QYVL59 PRELIMINARY; PRT: 426 AA.
 AC 08YTG9
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Hypothetical protein All2748.
 GN All2748.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 NCBI_Taxid=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; Pubmed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriuguchi W., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohata M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120";

RL DNA Res. 8:205-213(2001).
 DR EMBL; AP003590; BAB74447.1; -
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 13.
 DR PRINTS; PR01415; ANKXIN.
 DR SMART; SM00248; ANK; 13.
 DR PROSITE; PS50088; ANK_REPEAT; 11.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR KEGG; K04400; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 426 AA; 43800 MW; CF0B9E5D3ACAA03 CRC64;

Query Match 16.4%; Score 219.5; DB 16; Length 426;
 Best Local Similarity 30.7%; Pred. No. 3.5e-10;
 Matches 62; Conservative 34; Mismatches 71; Indels 35; Gaps 4;

QY 62 QAGSSLKHSSTL-----TNRGRNSVALPATLDSLSIHQAAQGEIDQK 107
 Db QGESALHLATVCGYDVVQVLNQGANTQIKNKGDTPLVALLQGH-----DQIV 285

QY 108 EHLRK-----GDNLVNKPDERGFTPLIMASAFGEIETVRELLMGADPHILAKERESAL 161
 Db ETLKXGANYHGDNL-----GETPLTASQGHATATVRLIDYGANANIPASDGKTL 338

QY 162 SLASTGCTDIYVGLLEERDVINITYDMNGTPTPLXAVGNHVCVEALLARGADLTTEAD 221
 Db 339 IKATERNHGVQLQLLAKGANVYQDSVGATATLIWAASGVNKKVQIILLEGADTNLKR 398

QY 222 SGYTPMDLVALGKRYKQVIE 243
 Db 399 GGYTALMIAPFNGFRSIVQLK 420

RESULT 6
 Q17344 PRELIMINARY; PRT; 1786 AA.
 ID AC Q17344
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE UNC-44 (Fragment).
 GN UNC-44.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodexinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RX MEDLINE=9526363; PubMed=7744957;
 RA Otsuka A., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y.,
 RA Boontarakulpoontawe P., Jeyapirakash A., Hedgecock E., Wheaton V.I.,
 RA Sobery A.;
 RT "An ankyrin-related gene (unc-44) is necessary for proper axonal
 RT guidance in *Caenorhabditis elegans*.";
 RL J. Cell Biol. 129:1081-1092(1995).
 DR EMBL; U21734; AA85854.1; -
 DR HSSP; P42773; 11HB.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001360; GH_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00023; ank; 24.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00791; ZU5; 1.
 DR SMART; SM00248; ANK; 21.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 22.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
 KW ANK repeat; Repeat.
 FT NON_TER 1786 1786

SQ SEQUENCE 1786 AA; 195550 MW; 03E220FB521747F1 CRC64;
 Query Match 16.0%; Score 214; DB 5; Length 1786;
 Best Local Similarity 27.3%; Pred. No. 8.7e-09;
 Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

QY 19 SELDPEDPGEADSGSTVTLSPCTREPVPNPEDASVSSPQAGSSLKHSSTLNNR 78
 Db 2 SNEBDPPQPOQOQESGEVQA-----PAAPFERAE----- 32

QY 79 GNEVSALPATLDSLSIHQAAQGEIDQKHLRKGDNLVKNPDERGFTPLIMASAFGEIE 138
 Db 33 -----GSASFIRARAGDLEKVELLRAGTD-INTSNANGINSLHASKGHSE 80

QY 139 TVRFLEMGADPHILAKERESALSLASTGCTTDYGLLERPVDINITYMNGSTPLIYAV 198
 Db 81 VRELIRQAVDPAATKRGNTALHIASLAGOSLIYTIIVENANVQSVNGFTPLYMAA 140

QY 199 RGNHVKCEALARGADLTTEADSGYTPMDLVALGY-RKYQVIE 244
 Db 141 QENHEEVKYLKKGANQALSTEDGFTPLVALVLLQGHDRVAVVLIEN 187

RESULT 7
 Q17487 PRELIMINARY; PRT; 1809 AA.
 ID AC Q17487
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE E. elegans ankyrin-related unc-44 (GB:U21734).
 GN UNC-44.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodexinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berts M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Faveilo A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., Murray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Riken L., Roopra A., Saunders D., Showkeen R.,
 RA Smaildon N., Smith A., Sonnenhammer E., Staden K., Sulston J.,
 RA Thierly-Mieg U., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Woldman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.*
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gattung S.;
 RT "The sequence of *C. elegans* cosmid B0350.";
 RL submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U50071; AAA93446.1; -
 DR HSSP; P42773; 11HB.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001360; GH_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00023; ank; 24.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01415; ANKXIN.
 DR SMART; SM00248; ANK; 21.
 DR SMART; SM00005; DEATH; 1.

DR SMART: SM00218; ZUS: 1.
 DR PROSITE: PS50088; ANK_REPEAT: 22.
 DR PROSITE: PS50297; ANK_REPEAT_REGION: 1.
 DR PROSITE: PS50017; DEATH_DOMAIN: 1.
 DR PROSITE: PS00572; GLYCOSYL_HYDROL_FL_1; UNKNOWN_2.
 DR ANK repeat: Repeat.
 KW ANK repeat: Repeat.
 SQ SEQUENCE 1809 AA; 198193 MW; AD86349AA64534F8 CRC64;

Query Match 16.0%; Score 214; DB 5; Length 1809;
 Best Local Similarity 27.3%; Pred. No. 8.9e-09;
 Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

DB 19 SELGDPEDEGEAAGSDTVVLSIFCTPEPVNPEPDASVSSPQAGSSLKSTLTITNRQ 78
 2 SNGGDPEPQPOQOPESEVQA---PAAPERGRAE----- 32

QY 79 GNEVSALPATLDSISIHQAAGELDQKEHLRKGDNLVKNPDERGFTPLWASAFGEIE 138
 33 -----GSASFRAARAGGLEKVELLRAGTD-INTSNANGLSLHLSKEGHS 80

QY 139 TVRFLEMGADPHILAKERESALSLASTGYTDIVGLLEPVDINIVDMNGTFLYAV 198
 DB 81 VVELLIRQAQVDATRKGNLTALHIASLAGOSLIVTIVENGANNVQSVNGFTPLWMAA 140

QY 199 RGNHVKCEVALLARGADLTTEADSGYTPMDLAVLGY-RKYQOVITEN 244
 DB 141 QENHEEVVKYLKHGANOALSTEDGFTPLAVALQOQHDRVAVLLEN 187

RESULT 8
 Q17488 PRELIMINARY; PRT; 1815 AA.

AC Q17488: 002517;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE C. ELEGANS ankyrin-related UNC-44 (GB:U21734).
 GN UNC-44.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RX MEDLINE=94150718; PubMed=7906398;
 RP SEQUENCE FROM N.A.
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 Lighting J., Lloyd C., Murray A., Mortimore B., O'Callaghan M.,
 Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showmken R.,
 Smailson N., Smith A., Sonhammer E., Staden R., Sulston J.,
 Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 Watson A., Weinstock L., Wilkinson-Sprat J., Whildan P., III of C.
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gattung S.,
 RN Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.,
 RN Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RX MEDLINE=95563663; PubMed=7744957;
 RA Otsuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y.,
 RA Bontrikulpontawe P., Jeyaprakash A., Hedgecock E., Wheaton V.I.,
 RA Sobery A.,

RT "An ankyrin-related gene (unc-44) is necessary for proper axonal
 RT guidance in Caenorhabditis elegans."
 RT J. Cell Biol. 129:1081-1092(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RA Otsuka A.J.,
 RA Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Otsuka A.J.,
 RN Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RL EMBL: U50071; AA93445.1;
 DR EMBL: U39847; AA841826.1;
 DR HSSP: P42773; 11HB.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR001360; Death.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR00906; ZUS.
 DR Pfam: PF00023; ank; 24.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00791; ZUS; 1.
 DR PRINTS: PR01415; ANKYRIN.
 DR SMART: SM00248; ANK; 21.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00218; ZUS; 1.
 DR PROSITE: PS50088; ANK_REPEAT: 22.
 DR PROSITE: PS50297; ANK_REPEAT_REGION: 1.
 DR PROSITE: PS50017; DEATH_DOMAIN: 1.
 DR PROSITE: PS00572; GLYCOSYL_HYDROL_FL_1; UNKNOWN_2.
 DR ANK repeat: Repeat.
 KW ANK repeat: Repeat.
 SQ SEQUENCE 1815 AA; 198956 MW; 3EC6E310915C915 CRC64;

Query Match 16.0%; Score 214; DB 5; Length 1815;
 Best Local Similarity 27.3%; Pred. No. 8.9e-09;
 Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

QY 19 SELGDPEDEGEAAGSDTVVLSIFCTPEPVNPEPDASVSSPQAGSSLKSTLTITNRQ 78
 DB 2 SNGGDPEPQPOQOPESEVQA---PAAPERGRAE----- 32

QY 79 GNEVSALPATLDSISIHQAAGELDQKEHLRKGDNLVKNPDERGFTPLWASAFGEIE 138
 DB 33 -----GSASFRAARAGGLEKVELLRAGTD-INTSNANGLSLHLSKEGHS 80

QY 139 TVRFLEMGADPHILAKERESALSLASTGYTDIVGLLEPVDINIVDMNGTFLYAV 198
 DB 81 VVELLIRQAQVDATRKGNLTALHIASLAGOSLIVTIVENGANNVQSVNGFTPLWMAA 140

QY 199 RGNHVKCEVALLARGADLTTEADSGYTPMDLAVLGY-RKYQOVITEN 244
 DB 141 QENHEEVVKYLKHGANOALSTEDGFTPLAVALQOQHDRVAVLLEN 187

RESULT 9
 Q17486 PRELIMINARY; PRT; 1867 AA.

AC Q17486: 002516;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE C. ELEGANS ankyrin-related UNC-44 (GB:U21734).
 GN UNC-44.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkhen R., Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Spratt J., Wohlman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans." Nature 368:32-38(1994).

SEQUENCE FROM N.A.
Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A.
STRAIN=N2;
MEDLINE=95263663; PubMed=7744957;
RA Otsuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y., Bonttrakulpoontawe P., Jeyaprasath A., Hedgecock E., Wheaton V.I., Sobery A.;
"An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in *Caenorhabditis elegans*." J. Cell Biol. 129:1081-1092(1995).
[5]
SEQUENCE FROM N.A.
STRAIN=N2;
Otsuka A.J.;
Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
STRAIN=N2;
Otsuka A.J.;
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RA EMBL; U50071; AAA93444.1;
RA EMBL; U39847; AAB41828.1;
RA HSSP; P42773; 11HB.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001360; GH 1.
DR InterPro; IPR000906; ZUS.
DR Pfam; PF00023; ank; 24.
DR Pfam; PF00531; death; 1.
DR PRINTS; PRO1415; ANKYRIN.
DR SMART; SM00248; ANK; 21.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS50088; ANK_REPEAT; 22.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
KW ANK repeat; Repeat.
SEQUENCE 1867 AA; 204253 MW; 4689A2104623B4C6 CRC64;

Query Match 16.0%; Score 214; DB 5; Length 1667;
Best Local Similarity 27.3%; Pred. No. 9.3e-09;
Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

19 SELGPDDEGGEAADSGTIVLSLFCPTPEPVNPEDASVSSPOAGSLKHSSTLTNR 78
2 SNEGDPDPPOQOQESQEVQA-----PAAPPEGRAR----- 32

79 GNEVSALPATLDSIHHOLAOGELDOUKHHRKGDNLVKNKDERGFTPLIASAFGEIE 138
33 -----GSASFLLAARAGDLEKVELLRAGTD-INTSNANGLSLHASKRGHSE 80

139 TWFLEWADPHILAKERESALASTGTYTDIVGLLLERVDVINYDMNGTPLLAV 198

DB 81 VRELIKROAQAADATRKNTALHIALAGOSLIVITLVENGANVWOSVNGFTPLVMA 140

QY 199 RGNHVCVEALLARGADLTTEADSGYTPMDLAVALCY-RKVOQVIN 244
DB 141 QNHHEVAVKYLKKGANQALSTEDGETPLAVALQGHDRVAVILN 187

RESULT 10
ID 017489 PRELIMINARY; PRT; 2039 AA.
AC 017489;
DT 01-NOV-1996 (TRENDBLREL 01, Created)
DT 01-NOV-1996 (TRENDBLREL 01, Last sequence update)
DT 01-JUN-2002 (TRENDBLREL 21, Last annotation update)
DE C. elegans ankyrin-related unc-44 (GB:U21734).
GN UNC-44.
OS *Caenorhabditis elegans*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; *Caenorhabditis*.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkhen R., Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Spratt J., Wohlman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans." Nature 368:32-38(1994).
[2]
RP SEQUENCE FROM N.A.
RA Gattung S.;
RT "The sequence of C. elegans cosmid B0350.";
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL; U50071; AAA93443.1;
RA HSSP; P42773; 11HB.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001360; GH 1.
DR InterPro; IPR000906; ZUS.
DR Pfam; PF00023; ank; 24.
DR Pfam; PF00531; death; 1.
DR PRINTS; PRO1415; ANKYRIN.
DR SMART; SM00248; ANK; 21.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS50088; ANK_REPEAT; 22.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
KW ANK repeat; Repeat.
SEQUENCE 2039 AA; 222850 MW; 7722C4C2B6AFD68A CRC64;

Query Match 16.0%; Score 214; DB 5; Length 2039;
Best Local Similarity 27.3%; Pred. No. 1.1e-08;
Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

19 SELGPDDEGGEAADSGTIVLSLFCPTPEPVNPEDASVSSPOAGSLKHSSTLTNR 78

Db 2 SNEGDEPPOQOQOPESEQVOA-----PAPEPGRAE----- 32

QY 79 GNEVSALPATLDSLSIHQAQGLDQKEHLRKGNLVNKPDERGFTPLIWSAFGEIE 138
 Db 33 -----GSASFLLRAARAGDLEKVELLRAGTD-INTSNANGINSIHLASKEGHS 80

QY 139 TYRFLLEWGDPHILAKESRSLASTGTYTDIVGLLERVDVINIYDNGGFTPLLYAV 198
 Db 81 VRELIRQAQVDAATRKNTALHIALAGOSLITVLIVENGANVQSVNGFTPLLYMAA 140

QY 199 RGNHVKCEVALLARAGADLTTEADSGYTPMDLAVALGY-RKVOQVIEN 244
 Db 141 QENHBEVVKYLLKKGANQALSTEDGFTPLAVALLQGHDRVAVALLLEN 187

RESULT 11

Q17343 PRELIMINARY; PRT; 6994 AA.

AC Q17343;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
 DE UNC-44 ankyrin.
 GN UNC-44.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peioderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RX MEDLINE=95263663; PubMed=7744957;
 RA Otsuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y.,
 RA Boontrakulponantawee P., Jayaprakash A., Hedgecock E., Wheaton V.I.,
 RA Sobey A.;
 RT "An ankyrin-related gene (unc-44) is necessary for proper axonal
 RT guidance in Caenorhabditis elegans.";
 RL J. Cell Biol. 129:1081-1092(1995).
 RN [2]
 RP REVISIONS, AND SEQUENCE OF 6126-6994 FROM N.A.
 RN RP STRAIN=N2;
 RA Otsuka A.J.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RL EMBL; U21733; AAB41827.1; -
 DR EMBL; U21733; AAB38384.1; -
 DR HSSP; P42773; 1IHB.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001360; GH_1.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR00906; ZUS-
 DR Pfam; PF00023; ank; 24.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00791; ZUS; 1.
 DR PRINTS; PRO1415; ANKYRIN.
 DR PRINTS; PRO0001; GLABLOOD.
 DR SMART; SM00248; ANK; 21.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00218; ZUS; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 22.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
 KW ANK repeat; Repeat.
 SEQUENCE 6994 AA; 775364 MW; 90CB449925D9923D CRC64;

Query Match 16.0%; Score 214; DB 5; Length 6994;
 Best Local Similarity 27.3%; Pred. No. 6,8e-08;
 Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

QY 19 SELGDEPGEAAAGSDTVVLSTFCTPEPVNPEPDASVSPQAGSLHSTTLNRR 78
 Db 2 SNEGDEPPOQOQOPESEQVOA-----PAPEPGRAE----- 32

QY 79 GNEVSALPATLDSLSIHQAQGLDQKEHLRKGNLVNKPDERGFTPLIWSAFGEIE 138
 Db 33 -----GSASFLLRAARAGDLEKVELLRAGTD-INTSNANGINSIHLASKEGHS 80

QY 139 TYRFLLEWGDPHILAKESRSLASTGTYTDIVGLLERVDVINIYDNGGFTPLLYAV 198
 Db 81 VRELIRQAQVDAATRKNTALHIALAGOSLITVLIVENGANVQSVNGFTPLLYMAA 140

QY 199 RGNHVKCEVALLARAGADLTTEADSGYTPMDLAVALGY-RKVOQVIEN 244
 Db 141 QENHBEVVKYLLKKGANQALSTEDGFTPLAVALLQGHDRVAVALLLEN 187

RESULT 12

Q9EOG6 PRELIMINARY; PRT; 1762 AA.

AC Q9EOG6;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-OCT-2001 (TEMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE KIDINS220.
 GN KIDINS220.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20568256; PubMed=10998417;
 RA Iglesias T., Cabrera-Poch N., Mitchell M.P., Naven T.J., Rozengurt E.,
 RA Schiavo G.;
 RT "Identification and cloning of Kidins220, a novel neuronal substrate
 RT of protein kinase D.";
 RL J. Biol. Chem. 275:40048-40056(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Schiavo G.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN RP SEQUENCE FROM N.A.
 RA Mitchell M., Schiavo G.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF239045; AAG35185.2; -
 DR HSSP; P80144; 2MYO.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 12.
 DR PRINTS; PRO1415; ANKYRIN.
 DR SMART; SM00248; ANK; 11.
 DR PROSITE; PS50088; ANK_REPEAT; 10.
 KW ANK repeat; Repeat.
 SEQUENCE 1762 AA; 195715 MW; 0CB2689A571F8AE4 CRC64;

Query Match 15.8%; Score 212; DB 11; Length 1762;
 Best Local Similarity 34.0%; Pred. No. 1,3e-08;
 Matches 50; Conservative 34; Mismatches 61; Indels 2; Gaps 2;

QY 100 QGBLDQKEHLRKGNLVNKPDERGFTPLIWSAFGEIEYRFLLEWGDPHILAKESR 159
 Db 81 EGHIIIVEELLKSGASLEHR-DWGGTALMWACYKGRDVEELLSHGANSVTLGYSVY 139

QY 160 ALSIATGTYTDIVGLLERVDVINIYDNGGFTPLLYAVRGNHVKCEVALLARAGADLTTE 219
 Db 140 PIIVAAGRGHADIVHLLONGAKVNCSDKGTPLVMAARGHLECVKHLAMGADVDE 199

QY 220 ADGTYTPMDLAVALGY-RKVOQVIEN 245
 Db 200 GANSMTLLIYAVKGYTQSVKEILKRN 226

RESULT 13

Q9ULH0 PRELIMINARY; PRT; 1777 AA.


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Db 1108 DKGFTPLLAATAGHVGVEIILLDNGADIEAQSERTKDTPLSLACSGGROEVVELLLAR 1167
QY 180 DVD---INIYDMNGSTPLLYAVRGNHVKCEALLARGADLTTEADS--GYTPMDLAVALG 234
Db 1168 GANKEHRNVSDY---TPLSLAASGYVNIKIILLNAGAEINSRTGSKGISPLMLAAMNG 1224
QY 235 Y 235
Db 1225 H 1225

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Search completed: March 17, 2003, 16:40:42
 Job time : 39 secs

